PAGE: 1

### RAW SEQUENCE LISTING PATENT APPLICATION US/08/386,680

DATE: 1 1/26/96 TIME: 17:52:45

This Raw Listing contains the General Information Section and up to the first 5 pages:

1	SEQUENCE LISTING	
2		
3	(1) General Information:	
<b>4</b> 5	(i) APPLICANT: Grotendorst, Gary R.	
6	Bradham Jr., Douglas M.,	
7	·	
8	(ii) TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR	R
9		
10	(iii) NUMBER OF SEQUENCES: 2	
11		
12	(iv) CORRESPONDENCE ADDRESS:	
13	(A) ADDRESSEE: Spensley Horn Jubas & Lubitz	
14	(B) STREET: 4225 Executive Square, Suite 1400	
15 16	(C) CITY: La Jolla (D) STATE: CA	
17	(E) COUNTRY: US	
18	(F) ZIP: 92037	
19	(2) 222 0 0 0 0	
20	(v) COMPUTER READABLE FORM:	
21	(A) MEDIUM TYPE: Floppy disk	
22	(B) COMPUTER: IBM PC compatible	
23	(C) OPERATING SYSTEM: PC-DOS/MS-DOS	
24	(D) SOFTWARE: PatentIn Release #1.0, Version #1.2	5
25		
26	(vi) CURRENT APPLICATION DATA:	
27	(A) APPLICATION NUMBER: US 08/386,680	
28	(B) FILING DATE: 10-FEB-1995	
29	(C) CLASSIFICATION: 435	
30 31	(vii) PRIOR APPLICATION DATA:	
32	(VII) PRIOR APPLICATION DATA:  (A) APPLICATION NUMBER: US/08/167,628	
33	(B) FILING DATE:	
34	(2) 22220 2222	
35	(A) APPLICATION NUMBER: US/07/752,427	
36	(B) FILING DATE:	
37		
38	(viii) ATTORNEY/AGENT INFORMATION:	
39	(A) NAME: Wetherell, Jr. Ph.D., John W.	
40	(B) REGISTRATION NUMBER: 31,678	
41	(C) REFERENCE/DOCKET NUMBER: PD-1294	
42		
43	(ix) TELECOMMUNICATION INFORMATION:	
44	(A) TELEPHONE: 619-455-5100	
45	(B) TELEFAX: 619-455-5110	
46		

# PAGE: 2 RAW SEQUENCE LISTING PATENT APPLICATION US/08/386,680

DATE: 11/26/96 TIME: 17:52:47

#### INPUT SET: S14073.raw

48 (2) INFORMATION FOR SEQ ID NO:1: 49 50 (i) SEQUENCE CHARACTERISTICS: 51 (A) LENGTH: 2075 base pairs 52 (B) TYPE: nucleic acid 53 (C) STRANDEDNESS: single 54 (D) TOPOLOGY: linear 55 56 (ii) MOLECULE TYPE: cDNA 57	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 2075 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: cDNA	
(A) LENGTH: 2075 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA	
52 (B) TYPE: nucleic acid 53 (C) STRANDEDNESS: single 54 (D) TOPOLOGY: linear 55 56 (ii) MOLECULE TYPE: cDNA	
(C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA	
(D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA	
55 56 (ii) MOLECULE TYPE: cDNA	
56 (ii) MOLECULE TYPE: cDNA	
<b>5</b> /	
58 59 (vii) IMMEDIATE SOURCE:	
60 (Vii) IMMEDIATE SOURCE: (B) CLONE: DB60R32	
61	
62 (ix) FEATURE:	
63 (A) NAME/KEY: CDS	
64 (B) LOCATION: 1301177	
65	
66	
67 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:	
68	
69 CCCGGCCGAC AGCCCCGAGA CGACAGCCCG GCGCGTCCCG GTCCCCACCT CC	GACCACCG 60
70	
71 CCAGCGCTCC AGGCCCCGCG CTCCCCGCTC GCCGCCACCG CGCCCTCCGC TC	CGCCCGCA 120
72	
73 GTGCCAACC ATG ACC GCC GCC AGT ATG GGC CCC GTC CGC GTC GCC	
Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala	Phe
75 1 5 10 - c	
76	AG MGG 216
77 GTG GTC CTC GCC CTC TGC AGC CGG CCG GCC GTC GGC CAG A	AC TGC 216
79 Uni Uni Inu Inu Xin Inu Oug Com Xmm Dro Xin Uni Ciu Cin X	
78 Val Val Leu Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln A	
79 15 20 25	
79 15 20 25 80	sn Cys
79 15 20 25 80 81 AGC GGG CCG TGC CGG TGC CCG GAC GAG CCG GCG CCG CGC TGC C	sn Cys CG GCG 264
79 15 20 25 80 81 AGC GGG CCG TGC CGG TGC CCG GAC GAG CCG GCG CCG CGC TGC C 82 Ser Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys P	sn Cys CG GCG 264
79 15 20 25 80 81 AGC GGG CCG TGC CGG TGC CCG GAC GAG CCG GCG CCG CGC TGC C 82 Ser Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys P	sn Cys CG GCG 264 Pro Ala
79 15 20 25 80 81 AGC GGG CCG TGC CGG TGC CCG GAC GAG CCG GCG CCG CGC TGC C 82 Ser Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys P 83 30 35 40	ecc ccc 264 Pro Ala 45
79 15 20 25 80 81 AGC GGG CCG TGC CGG TGC CCG GAC GAG CCG GCG CCG CGC TGC C 82 Ser Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys P 83 30 35 40	cc GCC 312
79       15       20       25         80       81       AGC GGG CCG TGC CGG TGC CCG GAC GAG CCG GCG CGC TGC CG         82       Ser Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys P         83       30       35         84         85       GGC GTG AGC CTC GTG CTG GAC GGC TGC GGC TGC TGC CGC GTC T	cc GCC 312
79 15 20 25 80 81 AGC GGG CCG TGC CGG TGC CCG GAC GAG CCG GCG CCG CGC TGC C 82 Ser Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys P 83 30 35 40 40 84 85 GGC GTG AGC CTC GTG CTG GAC GGC TGC GGC TGC CGC GTC TGC GGC GIV Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val C	cc cc 264 ro Ala 45 cc cc 312 ys Ala
79 15 20 25 80 81 AGC GGG CCG TGC CGG TGC CCG GAC GAG CCG GCG CCG CGC TGC CG82 Ser Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys P83 30 35 40 40 84 85 GGC GTG AGC CTC GTG CTG GAC GGC TGC GGC TGC CGC GTC TGC Gly Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val C87 50 55	CG GCG 264 Pro Ala 45 CGC GCC 312 Cys Ala 60
79 15 20 25 80 81 AGC GGG CCG TGC CGG TGC CCG GAC GAG CCG GCG CGC CGC TGC C 82 Ser Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys P 83 30 35 40 84 85 GGC GTG AGC CTC GTG CTG GAC GGC TGC GGC TGC CGC GTC T 86 Gly Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val C 87 50 55	CG GCG 264 Fro Ala 45 GC GCC 312 Sys Ala 60
79       15       20       25         80       81       AGC GGG CCG TGC CGG TGC CCG GAC GAG CCG GCG CGC CGC TGC CG       62       62       62       62       63	CG GCG 264 Fro Ala 45 GC GCC 312 Sys Ala 60
79       15       20       25         80       81       AGC GGG CCG TGC CGG TGC CCG GAC GAG CCG GCG CGC TGC CG       AGC CGG CGG CGG CGG CGG CGG CGG CGG CGG	CG GCG 264 Pro Ala 45 CG GCC 312 Cys Ala 60 CG CAC 360 Pro His
79       15       20       25         80       81       AGC GGG CCG TGC CGG TGC CCG GAC GAG CCG GCG CCG CGC TGC CG       62       62       62       62       62       62       63	CG GCG 264 Pro Ala 45 CG GCC 312 Cys Ala 60 CG CAC 360 Cro His
79       15       20       25         81       AGC GGG CCG TGC CGG TGC CGG TGC CGG GAC CGG CGG CGC TGC CG       CCG GAC GAG CCG GCG CGG CGC TGC CG         82       Ser Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Asp Gly Cys Gly Cys GGC TGC TGC CGC GTC TGC GGC GGC TGC TGC	CG GCG 264 Pro Ala 45 CG GCC 312 Cys Ala 60 CG CAC 360 Cro His
79       15       20       25 <td< td=""><td>CG GCG 264 Pro Ala 45 CG GCC 312 Cys Ala 60 CG CAC 360 Cro His</td></td<>	CG GCG 264 Pro Ala 45 CG GCC 312 Cys Ala 60 CG CAC 360 Cro His
79       15       20       25         81       AGC GGG CCG TGC CGG TGC CCG GAC GAC GAG CCG GCG CGC TGC CG       20       25         82       Ser Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Asp Gly Cys Gly Cys Cys Arg Cys Pro Asp Gly Cys Gly Cys Cys Arg Cys Arg Cys Pro Asp Gly Cys Gly Cys Cys Arg Cys Arg Cys Pro Asp Pro Cys Asp	CG GCG 264 Pro Ala 45 CG GCC 312 Cys Ala 60 CG CAC 360 Cro His CTC GGC 408 Cle Gly
79       15       20       25 <td< td=""><td>CG GCG 264 Pro Ala 45 CG GCC 312 Cys Ala 60 CG CAC 360 Cro His CTC GGC 408 Cle Gly CG GTG 456</td></td<>	CG GCG 264 Pro Ala 45 CG GCC 312 Cys Ala 60 CG CAC 360 Cro His CTC GGC 408 Cle Gly CG GTG 456

# PAGE: 3 RAW SEQUENCE LISTING PATENT APPLICATION US/08/386,680 TIME: 17:52:49

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101	ሞአሮ	מממ	<b>NGC</b>	GGY	GAG	TCC	ጥጥር	CAG	אממ	<b>NGC</b>	ጥርር	λλG	ሞልሮ	CAG	ጥርር	ACG	504
102						Ser								_		_	204
103	110	Arg	Der	Gry	OIG	115	Fire	GIN	Ser	Der	120	пур	- 7 -	0111	Cys	125	
104	140					110					140					123	
105	ጥርር	СПС	GAC	CCC	aca	GTG	aac	ጥርረ	<b>አ</b> ሞር	מממ	ርጥር	тас	ACC	ΔΨС	GAC	ርጥጥ	552
106						Val											332
107	Cys	пец	тэр	СТУ	130	Val	СТУ	Cys	Mec	135	пеа	Cys	Ser	Mec	140	Val	
108					130					133					740		
109	ር ር	СПС	מממ	λCC	ССФ	GAC	ጥርር	מממ	ጥጥረ	מממ	<b>ACC</b>	AGG	ርጥር	AAG	СПС	כככ	600
110						Asp							_				000
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112				110					100					100			
113	GGG	ΔΔΔ	TGC	TGC	GAG	GAG	ТGG	GTG	тст	GAC	GAG	CCC	AAG	GAC	CAA	ACC	648
114	_					Glu		_			_				_	_	
115	1	-1-	160	-1-				165	~ <i>1</i> ~	P			170				
116													_, ,				
117	GTG	GTT	GGG	ССТ	GCC	CTC	GCG	GCT	TAC	CGA	CTG	GAA	GAC	ACG	ттт	GGC	696
118			_			Leu						_		_	_	_	
119		175	1				180		-1-	5		185	<b>F</b>			2	
120																	
121	CCA	GAC	CCA	ACT	ATG	ATT	AGA	GCC	AAC	TGC	CTG	GTC	CAG	ACC	ACA	GAG	744
122	Pro	Asp	Pro	Thr	Met	Ile	Arq	Ala	Asn	Cys	Leu	Val	Gln	Thr	Thr	Glu	
123	190	-				195				•	200					205	
124																	
125	TGG	AGC	GCC	TGT	TCC	AAG	ACC	TGT	GGG	ATG	GGC	ATC	TCC	ACC	CGG	GTT	792
126	Trp	Ser	Ala	Cys	Ser	Lys	Thr	Cys	Gly	Met	Gly	Ile	Ser	Thr	Arg	Val	
127	_			_	210	_		_	_	215	_				220		
128																	
129	ACC	TAA	GAC	AAC	GCC	TCC	TGC	AGG	CTA	GAG	AAG	CAG	AGC	CGC	CTG	TGC	840
130	Thr	Asn	Asp	Asn	Ala	Ser	Cys	Arg	Leu	Glu	Lys	Gln	Ser	Arg	Leu	Cys	
131				225					230					235			
132																	
133	ATG	GTC	AGG	CCT	TGC	GAA	GCT	GAC	CTG	GAA	GAG	AAC	ATT	AAG	AAG	GGC	888
134	Met	Val	Arg	Pro	Cys	Glu	Ala	Asp	Leu	Glu	Glu	Asn	Ile	Lys	Lys	Gly	
135			240					245					250				
136																	
137	AAA	AAG	TGC	ATC	CGT	ACT	CCC	AAA	ATC	TCC	AAG	CCT	ATC	AAG	TTT	GAG	936
138	Lys	-	Cys	Ile	Arg	Thr		Lys	Ile	Ser	Lys		Ile	Lys	Phe	Glu	
139		255					260					265					
140																	
141						AGC											984
142		Ser	Gly	Cys	Thr	Ser	Met	Lys	Thr	Tyr		Ala	Lys	Phe	Cys		
143	270					275					280					285	
144	a=-	m <i></i> -		<b></b>	<i>~~</i>	~	<b>~</b> ~	<b>m</b>		<b>~~</b> ~	~-~					a= =	
145	_		_		_	CGA			_		_		_	_	_		1032
146	val	cys	rnr	Asp	_	Arg	cys	cys	unr		HlS	arg	Thr	Tnr		ьeu	
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148	~~~	ama.	<b>a.</b> a	mm~		maa	aam	<b>737</b>	~~~	<b>~</b> 3~	ama	3 m.a	~	2 2 ~	224	N III C	1000
149		_	_ )	_		TGC				_							1080
150	PIO	val	GTU		гÀ2	Cys	PIO	Asp		GTU	val	тэм	ьys		ASN	мет	
151				305					310					315			
152																	

### PAGE: 4 RAW SEQUENCE LISTING DATE: 11/26/96 PATENT APPLICATION US/08/386,680 TIME: 17:52:51

INPUT SET: S14073.raw ATG TTC ATC AAG ACC TGT GCC TGC CAT TAC AAC TGT CCC GGA GAC AAT Met Phe Ile Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn GAC ATC TTT GAA TCG CTG TAC TAC AGG AAG ATG TAC GGA GAC ATG GCA T Asp Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala GAAGCCAGAG AGTGAGAGAC ATTAACTCAT TAGACTGGAA CTTGAACTGA TTCACATCTC ATTTTTCCGT AAAAATGATT TCAGTAGCAC AAGTTATTTA AATCTGTTTT TCTAACTGGG GGAAAAGATT CCCACCCAAT TCAAAACATT GTGCCATGTC AAACAAATAG TCTATCTTCC CCAGACACTG GTTTGAAGAA TGTTAAGACT TGACAGTGGA ACTACATTAG TACACAGCAC CAGAATGTAT ATTAAGGTGT GGCTTTAGGA GCAGTGGGAG GGTACCGGCC CGGTTAGTAT CATCAGATCG ACTCTTATAC GAGTAATATG CCTGCTATTT GAAGTGTAAT TGAGAAGGAA AATTTTAGCG TGCTCACTGA CCTGCCTGTA GCCCCAGTGA CAGCTAGGAT GTGCATTCTC CAGCCATCAA GAGACTGAGT CAAGTTGTTC CTTAAGTCAG AACAGCAGAC TCAGCTCTGA CATTCTGATT CGAATGACAC TGTTCAGGAA TCGGAATCCT GTCGATTAGA CTGGACAGCT TGTGGCAAGT GAATTTGCCT GTAACAAGCC AGATTTTTTA AAATTTATAT TGTAAATATT GTGTGTGTGT GTGTGTGT ATATATATAT ATATATGTAC AGTTATCTAA GTTAATTTAA AGTTGTTTGT GCCTTTTTAT TTTTGTTTTT AATGCTTTGA TATTTCAATG TTAGCCTCAA TTTCTGAACA CCATAGGTAG AATGTAAAGC TTGTCTGATC GTTCAAAGCA TGAAATGGAT ACTTATATGG AAATTCTGCT CAGATAGAAT GACAGTCCGT CAAAACAGAT TGTTTGCAAA GGGGAGGCAT CAGTGTCTTG GCAGGCTGAT TTCTAGGTAG GAAATGTGGT AGCTCACG (2) INFORMATION FOR SEQ ID NO:2: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 349 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2: Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe Val Val Leu 

## PAGE: 5 RAW SEQUENCE LISTING PATENT APPLICATION US/08/386,680 TIME: 17:52:54

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										_					11 01	
206	Leu	Ala	Leu	Cys	Ser	Arg	Pro	Ala	Val	Gly	Gln	Asn	Cys	Ser	Gly	Pro
207				20					25					30		
208																
209	Cvs	Ara	Cvs	Pro	Asp	Glu	Pro	Ala	Pro	Ara	Cvs	Pro	Ala	Glv	Val	Ser
210	-1-	5	35		<u>F</u>			40		9	- <b>,</b> -		45	1		
			33					40					10			
211	<b>-</b>		T	*	<b>a</b> 1	<b>a</b>	<b>a1</b>	<b>~</b>	<b>a</b>	<b>3</b>	**-7	<b>a</b>	27.	¥	<b>a</b> 1 -	T
212	ren		Leu	Asp	GTÅ	cys	_	cys	cys	Arg	vaı		АТА	Lys	GIN	rea
213		50					55					60				
214																
215	Gly	Glu	Leu	Cys	Thr	Glu	Arg	Asp	Pro	Cys	Asp	Pro	His	Lys	Gly	Leu
216	65			_		70	_	_		_	75					80
217																
218	Phe	Cvs	Asn	Phe	G] v	Ser	Pro	Δla	Δsn	Δrα	T. 175	Tle	Glv	Val	Cvs	Thr
219	. 110	<b>C J D</b>	vob	1110	85	201	110	n_u	no	90	2,5	110	<b>0.1</b> 3	<b>7</b> G I	95	
					65					90					93	
220		_	_	<b>~</b> 3		_	<b>.</b>	-1.	-1	<b>~</b> 3 .	~~ 7	m1	7	<b>—</b>	•	<b>~</b>
221	А⊥а	Lys	Asp	_	АТа	Pro	cys	тте		GTA	стА	Thr	vaı	_	Arg	Ser
222				100					105					110		
223																
224	Gly	Glu	Ser	Phe	Gln	Ser	Ser	Cys	Lys	Tyr	Gln	Cys	Thr	Cys	Leu	Asp
225	_		115					120	_	_		_	125	_		_
226																
227	Glv	Δla	Val	Glv	Cvs	Met	Pro	Leu	Cvs	Ser	Met	Asp	Val	Ara	Leu	Pro
228	O+1	130	<b>7</b> G T	<b>0 1 1</b>	O J D	1100	135		0,0	501	1100	140	, u =	9	200	
		130					133					140				
229	<b>~</b>	D	3	<b>a</b>	D	D1	<b>D</b>	<b>3</b>	3	**- 7	T	T	D	<b>a</b> 1	T	<b>a</b>
230		Pro	ASP	cys	Pro		Pro	Arg	Arg	vaı	_	Leu	PIO	Gly	гàг	_
231	145					150					155					160
232																
233	Cys	Glu	Clu	m~~	t7_7	<b>A</b>	3	~1	D	T	3	~1 ~	mL	T 7 ~ 7	** - 3	~~~
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	-			-	165	<u>-</u>	_		_	170	_		_		175	_
235 236	-			Ala	165	<u>-</u>	_		Glu	170	_		_	Pro	175	_
235 236 237	-			-	165	<u>-</u>	_		_	170	_		_		175	_
235 236 237 238	Pro	Ala	Leu	Ala 180	165 Ala	Tyr	Arg	Leu	Glu 185	170 Asp	Thr	Phe	Gly	Pro 190	175 Asp	Pro
235 236 237 238 239	Pro	Ala	Leu Ile	Ala 180	165 Ala	Tyr	Arg	Leu Leu	Glu 185	170 Asp	Thr	Phe	Gly Glu	Pro 190	175 Asp	_
235 236 237 238 239 240	Pro	Ala	Leu	Ala 180	165 Ala	Tyr	Arg	Leu	Glu 185	170 Asp	Thr	Phe	Gly	Pro 190	175 Asp	Pro
235 236 237 238 239 240 241	Pro Thr	Ala Met	Leu Ile 195	Ala 180 Arg	165 Ala Ala	Tyr Asn	Arg Cys	Leu Leu 200	Glu 185 Val	170 Asp Gln	Thr Thr	Phe Thr	Gly Glu 205	Pro 190 Trp	175 Asp Ser	Pro
235 236 237 238 239 240 241 242	Pro Thr	Ala Met Ser	Leu Ile 195	Ala 180 Arg	165 Ala Ala	Tyr Asn	Arg Cys Met	Leu Leu 200	Glu 185 Val	170 Asp Gln	Thr Thr	Phe Thr	Gly Glu 205	Pro 190 Trp	175 Asp Ser	Pro
235 236 237 238 239 240 241 242 243	Pro Thr	Ala Met	Leu Ile 195	Ala 180 Arg	165 Ala Ala	Tyr Asn	Arg Cys	Leu Leu 200	Glu 185 Val	170 Asp Gln	Thr Thr	Phe Thr	Gly Glu 205	Pro 190 Trp	175 Asp Ser	Pro
235 236 237 238 239 240 241 242	Pro Thr	Ala Met Ser	Leu Ile 195	Ala 180 Arg	165 Ala Ala	Tyr Asn	Arg Cys Met	Leu Leu 200	Glu 185 Val	170 Asp Gln	Thr Thr	Phe Thr	Gly Glu 205	Pro 190 Trp	175 Asp Ser	Pro
235 236 237 238 239 240 241 242 243	Pro Thr	Ala Met Ser 210	Leu Ile 195 Lys	Ala 180 Arg	165 Ala Ala Cys	Tyr Asn Gly	Arg Cys Met 215	Leu 200 Gly	Glu 185 Val	170 Asp Gln Ser	Thr Thr	Phe Thr Arg 220	Glu 205 Val	Pro 190 Trp	175 Asp Ser Asn	Pro Ala Asp
235 236 237 238 239 240 241 242 243 244	Pro Thr	Ala Met Ser 210	Leu Ile 195 Lys	Ala 180 Arg	165 Ala Ala Cys	Tyr Asn Gly	Arg Cys Met 215	Leu 200 Gly	Glu 185 Val	170 Asp Gln Ser	Thr Thr	Phe Thr Arg 220	Glu 205 Val	Pro 190 Trp	175 Asp Ser Asn	Pro Ala Asp
235 236 237 238 239 240 241 242 243 244 245 246	Pro Thr Cys	Ala Met Ser 210	Leu Ile 195 Lys	Ala 180 Arg	165 Ala Ala Cys	Tyr Asn Gly Leu	Arg Cys Met 215	Leu 200 Gly	Glu 185 Val	170 Asp Gln Ser	Thr Thr Thr	Phe Thr Arg 220	Glu 205 Val	Pro 190 Trp	175 Asp Ser Asn	Pro Ala Asp
235 236 237 238 239 240 241 242 243 244 245 246 247	Pro Thr Cys Asn 225	Ala Met Ser 210 Ala	Leu Ile 195 Lys Ser	Ala 180 Arg Thr	165 Ala Ala Cys	Tyr Asn Gly Leu 230	Arg Cys Met 215	Leu 200 Gly	Glu 185 Val Ile Gln	170 Asp Gln Ser	Thr Thr Arg 235	Phe Thr Arg 220 Leu	Glu 205 Val	Pro 190 Trp Thr	175 Asp Ser Asn	Pro Ala Asp Arg 240
235 236 237 238 239 240 241 242 243 244 245 246 247 248	Pro Thr Cys Asn 225	Ala Met Ser 210 Ala	Leu Ile 195 Lys Ser	Ala 180 Arg Thr	165 Ala Ala Cys Arg	Tyr Asn Gly Leu 230	Arg Cys Met 215	Leu 200 Gly	Glu 185 Val Ile Gln	170 Asp Gln Ser Ile	Thr Thr Arg 235	Phe Thr Arg 220 Leu	Glu 205 Val	Pro 190 Trp	175 Asp Ser Asn Val	Pro Ala Asp Arg 240
235 236 237 238 239 240 241 242 243 244 245 246 247 248 249	Pro Thr Cys Asn 225	Ala Met Ser 210 Ala	Leu Ile 195 Lys Ser	Ala 180 Arg Thr	165 Ala Ala Cys	Tyr Asn Gly Leu 230	Arg Cys Met 215	Leu 200 Gly	Glu 185 Val Ile Gln	170 Asp Gln Ser	Thr Thr Arg 235	Phe Thr Arg 220 Leu	Glu 205 Val	Pro 190 Trp Thr	175 Asp Ser Asn	Pro Ala Asp Arg 240
235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250	Pro Thr Cys Asn 225 Pro	Ala Met Ser 210 Ala Cys	Leu Ile 195 Lys Ser	Ala 180 Arg Thr Cys	Ala Ala Cys Arg Asp 245	Tyr Asn Gly Leu 230 Leu	Arg Cys Met 215 Glu	Leu 200 Gly Lys	Glu 185 Val Ile Gln	170 Asp Gln Ser Ile 250	Thr Thr Arg 235 Lys	Phe Thr Arg 220 Leu Lys	Gly Glu 205 Val Cys	Pro 190 Trp Thr Met	175 Asp Ser Asn Val Lys 255	Pro Ala Asp Arg 240 Cys
235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251	Pro Thr Cys Asn 225 Pro	Ala Met Ser 210 Ala Cys	Leu Ile 195 Lys Ser	Ala 180 Arg Thr Cys Ala	Ala Ala Cys Arg Asp 245	Tyr Asn Gly Leu 230 Leu	Arg Cys Met 215 Glu	Leu 200 Gly Lys	Glu 185 Val Ile Gln Asn	170 Asp Gln Ser Ile 250	Thr Thr Arg 235 Lys	Phe Thr Arg 220 Leu	Gly Glu 205 Val Cys	Pro 190 Trp Thr Met Lys	175 Asp Ser Asn Val Lys 255	Pro Ala Asp Arg 240 Cys
235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252	Pro Thr Cys Asn 225 Pro	Ala Met Ser 210 Ala Cys	Leu Ile 195 Lys Ser	Ala 180 Arg Thr Cys	Ala Ala Cys Arg Asp 245	Tyr Asn Gly Leu 230 Leu	Arg Cys Met 215 Glu	Leu 200 Gly Lys	Glu 185 Val Ile Gln	170 Asp Gln Ser Ile 250	Thr Thr Arg 235 Lys	Phe Thr Arg 220 Leu	Gly Glu 205 Val Cys	Pro 190 Trp Thr Met	175 Asp Ser Asn Val Lys 255	Pro Ala Asp Arg 240 Cys
235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251	Pro Thr Cys Asn 225 Pro	Ala Met Ser 210 Ala Cys	Leu Ile 195 Lys Ser	Ala 180 Arg Thr Cys Ala	Ala Ala Cys Arg Asp 245	Tyr Asn Gly Leu 230 Leu	Arg Cys Met 215 Glu	Leu 200 Gly Lys	Glu 185 Val Ile Gln Asn	170 Asp Gln Ser Ile 250	Thr Thr Arg 235 Lys	Phe Thr Arg 220 Leu	Gly Glu 205 Val Cys	Pro 190 Trp Thr Met Lys	175 Asp Ser Asn Val Lys 255	Pro Ala Asp Arg 240 Cys
235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252	Pro Thr Cys Asn 225 Pro	Ala Met Ser 210 Ala Cys	Leu Ile 195 Lys Ser Glu	Ala 180 Arg Thr Cys Ala Pro 260	Ala Ala Cys Arg Asp 245 Lys	Tyr Asn Gly Leu 230 Leu	Arg Cys Met 215 Glu Glu	Leu 200 Gly Lys	Glu 185 Val Ile Gln Asn Pro 265	170 Asp Gln Ser Ile 250 Ile	Thr Thr Arg 235 Lys	Phe Thr Arg 220 Leu Lys	Glu 205 Val Cys Gly	Pro 190 Trp Thr Met Lys	Asp Ser Asn Val Lys 255 Ser	Pro Ala Asp Arg 240 Cys
235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253	Pro Thr Cys Asn 225 Pro	Ala Met Ser 210 Ala Cys	Leu Ile 195 Lys Ser Glu	Ala 180 Arg Thr Cys Ala Pro 260	Ala Ala Cys Arg Asp 245 Lys	Tyr Asn Gly Leu 230 Leu	Arg Cys Met 215 Glu Glu	Leu 200 Gly Lys	Glu 185 Val Ile Gln Asn Pro 265	170 Asp Gln Ser Ile 250 Ile	Thr Thr Arg 235 Lys	Phe Thr Arg 220 Leu Lys	Glu 205 Val Cys Gly	Pro 190 Trp Thr Met Lys Leu 270	Asp Ser Asn Val Lys 255 Ser	Pro Ala Asp Arg 240 Cys
235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254	Pro Thr Cys Asn 225 Pro	Ala Met Ser 210 Ala Cys	Leu Ile 195 Lys Ser Glu Thr	Ala 180 Arg Thr Cys Ala Pro 260	Ala Ala Cys Arg Asp 245 Lys	Tyr Asn Gly Leu 230 Leu	Arg Cys Met 215 Glu Glu	Leu 200 Gly Lys Glu Arg	Glu 185 Val Ile Gln Asn Pro 265	170 Asp Gln Ser Ile 250 Ile	Thr Thr Arg 235 Lys	Phe Thr Arg 220 Leu Lys	Gly Glu 205 Val Cys Gly Glu	Pro 190 Trp Thr Met Lys Leu 270	Asp Ser Asn Val Lys 255 Ser	Pro Ala Asp Arg 240 Cys
235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 256	Pro Thr Cys Asn 225 Pro Ile Cys	Ala Met Ser 210 Ala Cys Arg	Leu Ile 195 Lys Ser Glu Thr	Ala 180 Arg Thr Cys Ala Pro 260 Met	Ala Ala Cys Arg Asp 245 Lys Lys	Tyr Asn Gly Leu 230 Leu Thr	Arg Cys Met 215 Glu Glu Ser	Leu 200 Gly Lys Glu Lys	Glu 185 Val Ile Gln Asn Pro 265 Ala	170 Asp Gln Ser Ile 250 Ile Lys	Thr Thr Arg 235 Lys Phe	Phe Thr Arg 220 Leu Lys Phe Cys	Glu 205 Val Cys Gly Glu Gly 285	Pro 190 Trp Thr Met Lys Leu 270 Val	Asp Ser Asn Val Lys 255 Ser Cys	Pro Ala Asp Arg 240 Cys Gly Thr
235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 255	Pro Thr Cys Asn 225 Pro Ile Cys	Ala Met Ser 210 Ala Cys Arg	Leu Ile 195 Lys Ser Glu Thr	Ala 180 Arg Thr Cys Ala Pro 260 Met	Ala Ala Cys Arg Asp 245 Lys Lys	Tyr Asn Gly Leu 230 Leu Thr	Arg Cys Met 215 Glu Glu Ser	Leu 200 Gly Lys Glu Lys	Glu 185 Val Ile Gln Asn Pro 265 Ala	170 Asp Gln Ser Ile 250 Ile Lys	Thr Thr Arg 235 Lys Phe	Phe Thr Arg 220 Leu Lys Phe Cys	Glu 205 Val Cys Gly Glu Gly 285	Pro 190 Trp Thr Met Lys Leu 270	Asp Ser Asn Val Lys 255 Ser Cys	Pro Ala Asp Arg 240 Cys Gly Thr

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